



SEQUENCE LISTING

<110> John E. THOMPSON et al.

<120> DNA ENCODING A PLANT LIPASE,

TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESCENCE IN
PLANTS

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<140> 09/610,104

<141> 2000-07-05

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<151> 2000-06-09

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<151> 1998-06-26

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Glu Ala Gln Pro Leu Gly Leu Ser Lys Pro Gly Pro Thr Trp Pro Glu
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Leu Leu Gly Ser Asn Ala Trp Ala Gly Leu Leu Asn Pro Leu Asn Asp
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gag ctc cgt gag ctc ctc cta cgc tgc ggg gac ttc tgc cag gtg aca   200
Glu Leu Arg Glu Leu Leu Arg Cys Gly Asp Phe Cys Gln Val Thr
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Arg	Tyr	Gly	Lys	Ala	Asp	Leu	Leu	His	Lys	Thr	Ala	Phe	Pro	Gly	Gly		
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gca	gac	cgg	ttt	gac	gtg	gtg	gcg	tac	ttg	tac	gcc	act	gcg	aag	gtc	344	
Ala	Asp	Arg	Phe	Asp	Val	Val	Ala	Tyr	Leu	Tyr	Ala	Thr	Ala	Lys	Val		
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agc	gtc	cca	gag	gcg	ttt	ctg	ctg	aag	tcg	agg	tcg	agg	gag	aag	tgg	392	
Ser	Val	Pro	Glu	Ala	Phe	Leu	Leu	Lys	Ser	Arg	Ser	Arg	Glu	Lys	Trp		
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Asp	Arg	Glu	Ser	Asn	Trp	Ile	Gly	Tyr	Val	Val	Val	Ser	Asn	Asp	Glu		
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Thr	Ser	Arg	Val	Ala	Gly	Arg	Arg	Glu	Val	Tyr	Val	Val	Trp	Arg	Gly		
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Ser	Ala	His	Pro	Leu	Leu	Arg	Thr	Gln	Gln	Thr	Thr	His	Val	Glu	Lys		
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Val	Glu	Asn	Glu	Glu	Lys	Lys	Ser	Ile	His	Lys	Ser	Ser	Trp	Tyr	Asp		
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Cys	Phe	Asn	Ile	Asn	Leu	Leu	Gly	Ser	Ala	Ser	Lys	Asp	Lys	Gly	Lys		
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gga	agc	gac	gac	gac	gat	gat	gac	gac	ccc	aaa	gtg	atg	caa	ggt	tgg	728	
Gly	Ser	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Pro	Lys	Val	Met	Gln	Gly	Trp		
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Met	Thr	Ile	Tyr	Thr	Ser	Glu	Asp	Pro	Lys	Ser	Pro	Phe	Thr	Lys	Leu		
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agt	gca	aga	aca	caa	ctt	cag	acc	aaa	ctc	aaa	caa	cta	atg	aca	aaa	824	
Ser	Ala	Arg	Thr	Gln	Leu	Gln	Thr	Lys	Leu	Lys	Gln	Leu	Met	Thr	Lys		
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Tyr	Lys	Asp	Glu	Thr	Leu	Ser	Ile	Thr	Phe	Ala	Gly	His	Ser	Leu	Gly		
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Ala Thr Leu Ser Val Val Ser Ala Phe Asp Ile Val Glu Asn Leu Thr	
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Thr Glu Ile Pro Val Thr Ala Val Val Phe Gly Cys Pro Lys Val Gly	
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aac aaa aaa ttc caa caa ctc ttc gac tcg tac cca aac cta aat gtc	1016
Asn Lys Lys Phe Gln Gln Leu Phe Asp Ser Tyr Pro Asn Leu Asn Val	
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ctc cat gta agg aat gtc atc gac ctg atc cct ctg tat ccc gtg aaa	1064
Leu His Val Arg Asn Val Ile Asp Leu Ile Pro Leu Tyr Pro Val Lys	
325 330 335	
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Leu Met Gly Tyr Val Asn Ile Gly Ile Glu Leu Glu Ile Asp Ser Arg	
340 345 350 355	
aag tcg acc ttt cta aag gac tcg aaa aac ccg agt gat tgg cat aat	1160
Lys Ser Thr Phe Leu Lys Asp Ser Lys Asn Pro Ser Asp Trp His Asn	
360 365 370	
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Leu Gln Ala Ile Leu His Val Val Ser Gly Trp His Gly Val Lys Gly	
375 380 385	
gag ttt aag gtt gta aat aag aga agt gtt gca ttg gtt aat aag tca	1256
Glu Phe Lys Val Val Asn Lys Arg Ser Val Ala Leu Val Asn Lys Ser	
390 395 400	
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Cys Asp Phe Leu Lys Glu Glu Cys Leu Val Pro Pro Ala Trp Trp Val	
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Val Gln Asn Lys Gly Met Val Leu Asn Lys Asp Gly Glu Trp Val Leu	
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aac gat gag gat gag gac gag gac gag gat gag atc aaa gta atg gat 146
Asn Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Ile Lys Val Met Asp
35 40 45

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Gly	Trp	Leu	Lys	Ile	Tyr	Val	Ser	Ser	Asn	Pro	Lys	Ser	Ser	Phe	Thr	
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Arg	Leu	Ser	Ala	Arg	Glu	Gln	Leu	Gln	Ala	Lys	Ile	Glu	Lys	Leu	Arg	
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Asn	Glu	Tyr	Lys	Asp	Glu	Asn	Leu	Ser	Ile	Thr	Phe	Thr	Gly	His	Ser	
		80			85				90						95	
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ggt	gtg	cca	gtt	gat	att	cca	gta	tct	gca	att	gta	ttt	ggt	agt	cca	386
Gly	Val	Pro	Val	Asp	Ile	Pro	Val	Ser	Ala	Ile	Val	Phe	Gly	Ser	Pro	
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Gln	Val	Gly	Asn	Lys	Ala	Phe	Asn	Glu	Arg	Ile	Lys	Lys	Phe	Ser	Asn	
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ttg	aat	atc	tta	cat	gtt	aag	aac	aag	att	gat	ctc	att	acc	ctt	tac	482
Leu	Asn	Ile	Leu	His	Val	Lys	Asn	Lys	Ile	Asp	Leu	Ile	Thr	Leu	Tyr	
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cca	agt	gct	ctg	ttt	ggg	tat	gtg	aat	tca	ggtattgaag	gaaaagatca					532
Pro	Ser	Ala	Leu	Phe	Gly	Tyr	Val	Asn	Ser							
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catatgagaa	atcaacactc	tactaacttt	atgctataag	agaatagggt	aaggtccata											712
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attcttcaac	a ggt	ata gag	cta gtc	atc gat	agc aga	aag tct	ccg agt									882
	Gly	Ile	Glu	Leu	Val	Ile	Asp	Ser	Arg	Lys	Ser	Pro	Ser			
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 35 40 45
 Gln Val Thr Tyr Asp Thr Phe Ile Asn Asp Gln Asn Ser Ser Tyr Cys
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 Gly Ser Ser Arg Tyr Gly Lys Ala Asp Leu Leu His Lys Thr Ala Phe
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 Pro Gly Gly Ala Asp Arg Phe Asp Val Val Ala Tyr Leu Tyr Ala Thr
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 Ala Lys Val Ser Val Pro Glu Ala Phe Leu Leu Lys Ser Arg Ser Arg
 100 105 110
 Glu Lys Trp Asp Arg Glu Ser Asn Trp Ile Gly Tyr Val Val Val Ser
 115 120 125
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 130 135 140
 Trp Arg Gly Thr Cys Arg Asp Tyr Glu Trp Val Asp Val Leu Gly Ala

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Gln	Leu	Glu	Ser	Ala	His	Pro
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Val	Glu	Lys	Val	Glu	Asn	Glu
				180		185
Trp	Tyr	Asp	Cys	Phe	Asn	Ile
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Lys	Gly	Lys	Gly	Ser	Asp	Asp
				210		215
Gln	Gly	Trp	Met	Thr	Ile	Tyr
				225		230
Thr	Lys	Leu	Ser	Ala	Arg	Thr
				245		250
Met	Thr	Lys	Tyr	Lys	Asp	Glu
				260		265
Ser	Leu	Gly	Ala	Thr	Leu	Ser
				275		280
Asn	Leu	Thr	Thr	Glu	Ile	Pro
				290		295
Lys	Val	Gly	Asn	Lys	Lys	Phe
				305		310
Leu	Asn	Val	Leu	His	Val	Arg
				325		330
Pro	Val	Lys	Leu	Met	Gly	Tyr
				340		345
Asp	Ser	Arg	Lys	Ser	Thr	Phe
				355		360
Trp	His	Asn	Leu	Gln	Ala	Ile
				370		375
Val	Lys	Gly	Glu	Phe	Lys	Val
				385		390
Asn	Lys	Ser	Cys	Asp	Phe	Leu
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Trp	Trp	Val	Val	Gln	Asn	Lys
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Trp	Val	Leu	Ala	Pro	Pro	Glu
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 35 40 45
 His Tyr Gly Glu Met Ala Gln Ala Gly Tyr Asp Thr Phe Asn Ile Asn
 50 55 60
 Thr Glu Ser Gln Phe Ala Gly Ala Ser Ile Tyr Ser Arg Lys Asp Phe
 65 70 75 80
 Phe Ala Lys Val Gly Leu Glu Ile Ala His Pro Tyr Thr Lys Tyr Lys

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Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile			
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Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp			
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Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe			
65	70	75	80
Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr			
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Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser			
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Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val			
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Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp			
130	135	140	
Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala			
145	150	155	160
Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys			
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Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr			
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Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln			
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Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp			
210	215	220	
Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala			
225	230	235	240
Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg			
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Ser Lys Lys Gly Lys Val Ile Pro Val Thr Ala Val Leu Thr Tyr Gly			
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Gly Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu			
275	280	285	
Gly Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys			
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Ser Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys			
305	310	315	320
Ile Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu			
325	330	335	
Ala Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val			
340	345	350	
Ser Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr			
355	360	365	
His Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala			
370	375	380	
Leu Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro			
385	390	395	400
Pro Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu			
405	410	415	
Gly Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser			
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 Asn Phe Leu Tyr Ala Thr Ala Arg Val Ser Leu Pro Glu Gly Leu Leu
 20 25 30

ctc caa tca caa tca aga gat tct tgg gac cgt gag tct aac tgg ttt 144
 Leu Gln Ser Gln Ser Arg Asp Ser Trp Asp Arg Glu Ser Asn Trp Phe
 35 40 45

ggc tac att gct gtc acg tct gat gaa cgg tct aag gct tta gga cgc 192
 Gly Tyr Ile Ala Val Thr Ser Asp Glu Arg Ser Lys Ala Leu Gly Arg
 50 55 60

cgt gag atc tat ata gct ttg aga gga acg agc agg aac tat gag tgg 240
 Arg Glu Ile Tyr Ile Ala Leu Arg Gly Thr Ser Arg Asn Tyr Glu Trp
 65 70 75 80

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 Val Asn Val Leu Gly Ala Arg Pro Thr Ser Ala Asp Pro Leu Leu His
 85 90 95

gga ccc gag cag gat ggt tct ggt ggt gta gtt gaa ggt acg act ttt 336
 Gly Pro Glu Gln Asp Gly Ser Gly Gly Val Val Glu Gly Thr Thr Phe
 100 105 110

gat agt gac agt gaa gat gaa gaa ggg tgt aag gtg atg ctc ggg tgg 384
 Asp Ser Asp Ser Glu Asp Glu Glu Gly Cys Lys Val Met Leu Gly Trp
 115 120 125

ctc aca atc tat act tct aat cac ccc gaa tcc aaa ttc act aag ctg 432
 Leu Thr Ile Tyr Thr Ser Asn His Pro Glu Ser Lys Phe Thr Lys Leu
 130 135 140

agt cta cgg tca cag ttg tta gcc aag atc aag gag ctt ctg ttg aag 480
 Ser Leu Arg Ser Gln Leu Leu Ala Lys Ile Lys Glu Leu Leu Leu Lys
 145 150 155 160

tat aag gac gag aaa ccg agc att gtg ttg act gga cat agc ttg gga 528
 Tyr Lys Asp Glu Lys Pro Ser Ile Val Leu Thr Gly His Ser Leu Gly
 165 170 175

cct aca gag gct gtt ctg gcc gcc tat gat ata gct gag aac ggt tcc 576
 Pro Thr Glu Ala Val Leu Ala Ala Tyr Asp Ile Ala Glu Asn Gly Ser

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195	200	205	
gga aac aag gag ttc aga gac gaa gta atg agt cac aag aac tta aag			672
Gly Asn Lys Glu Phe Arg Asp	Glu Val Met Ser	His Lys Asn Leu Lys	
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gga ctt tta ggg tat gtg gac ata gga ata aac ttt gtg atc gat aca			768
Gly Leu Leu Gly Tyr Val Asp	Ile Gly Ile Asn Phe Val	Ile Asp Thr	
245	250	255	
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Lys Lys Ser Pro Phe Leu Ser Asp	Ser Arg Asn Pro Gly Asp	Trp His	
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Asn Leu Gln Ala Met Leu His	Val Val Ala Gly Trp Asn Gly Lys Lys		
275	280	285	
gga gag ttt aaa ctg atg gtt aag aga agt att gca tta gtg aac aag			912
Gly Glu Phe Lys Leu Met Val	Lys Arg Ser Ile Ala Leu Val Asn Lys		
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Ser Cys Glu Phe Leu Lys Ala Glu Cys Leu Val Pro Gly Ser Trp Trp			
305	310	315 320	
gta gag aag aac aaa gga ctg atc aag aac gaa gat ggt gaa tgg gtt			1008
Val Glu Lys Asn Lys Gly Leu Ile Lys Asn Glu Asp Gly Glu Trp Val			
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Gly Tyr Ile Ala Val Thr Ser Asp Glu Arg Ser Lys Ala Leu Gly Arg		
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Arg Glu Ile Tyr Ile Ala Leu Arg Gly Thr Ser Arg Asn Tyr Glu Trp		
65	70	75
Val Asn Val Leu Gly Ala Arg Pro Thr Ser Ala Asp Pro Leu Leu His		
85	90	95
Gly Pro Glu Gln Asp Gly Ser Gly Gly Val Val Glu Gly Thr Thr Phe		
100	105	110
Asp Ser Asp Ser Glu Asp Glu Glu Gly Cys Lys Val Met Leu Gly Trp		
115	120	125
Leu Thr Ile Tyr Thr Ser Asn His Pro Glu Ser Lys Phe Thr Lys Leu		
130	135	140
Ser Leu Arg Ser Gln Leu Leu Ala Lys Ile Lys Glu Leu Leu Leu Lys		
145	150	155
Tyr Lys Asp Glu Lys Pro Ser Ile Val Leu Thr Gly His Ser Leu Gly		
165	170	175
Pro Thr Glu Ala Val Leu Ala Ala Tyr Asp Ile Ala Glu Asn Gly Ser		
180	185	190
Ser Asp Asp Val Pro Val Thr Ala Ile Val Phe Gly Cys Pro Gln Val		
195	200	205
Gly Asn Lys Glu Phe Arg Asp Glu Val Met Ser His Lys Asn Leu Lys		
210	215	220
Ile Leu His Val Arg Asn Thr Ile Asp Leu Leu Thr Arg Tyr Pro Gly		
225	230	235
Gly Leu Leu Gly Tyr Val Asp Ile Gly Ile Asn Phe Val Ile Asp Thr		
245	250	255
Lys Lys Ser Pro Phe Leu Ser Asp Ser Arg Asn Pro Gly Asp Trp His		
260	265	270
Asn Leu Gln Ala Met Leu His Val Val Ala Gly Trp Asn Gly Lys Lys		
275	280	285
Gly Glu Phe Lys Leu Met Val Lys Arg Ser Ile Ala Leu Val Asn Lys		
290	295	300
Ser Cys Glu Phe Leu Lys Ala Glu Cys Leu Val Pro Gly Ser Trp Trp		
305	310	315
Val Glu Lys Asn Lys Gly Leu Ile Lys Asn Glu Asp Gly Glu Trp Val		
325	330	335
Leu Ala Pro Val Glu Glu Glu Pro Val Pro Glu Phe		
340	345	

<210> 17
 <211> 195
 <212> PRT
 <213> Plant

<400> 17
 Asp Tyr Glu Trp Val Asp Val Leu Gly Ala Arg Pro Asp Ser Ala Asp
 1 5 10 15
 Ser Leu Leu His Pro Lys Ser Leu Gln Lys Gly Ile Asn Asn Lys Asn
 20 25 30
 Asp Glu Asp Glu Asp Glu Asp Glu Ile Lys Val Met Asp Gly
 35 40 45
 Trp Leu Lys Ile Tyr Val Ser Asn Pro Lys Ser Ser Phe Thr Arg
 50 55 60
 Leu Ser Ala Arg Glu Gln Leu Gln Ala Lys Ile Glu Lys Leu Arg Asn

65		70		75		80
Glu Tyr Lys Asp	Glu Asn Leu Ser Ile Thr Phe Thr Gly His Ser Leu					
	85		90		95	
Gly Ala Ser Leu Ala Val Leu Ala Ser Phe Asp Val Val Glu Asn Gly						
	100		105		110	
Val Pro Val Asp Ile Pro Val Ser Ala Ile Val Phe Gly Ser Pro Gln						
	115		120		125	
Val Gly Asn Lys Ala Phe Asn Glu Arg Ile Lys Lys Phe Ser Asn Leu						
	130		135		140	
Asn Ile Leu His Val Lys Asn Lys Ile Asp Leu Ile Thr Leu Tyr Pro						
145		150		155		160
Ser Ala Leu Phe Gly Tyr Val Asn Ser Gly Ile Glu Leu Val Ile Asp						
	165		170		175	
Ser Arg Lys Ser Pro Ser Leu Lys Asp Ser Lys Asp Met Gly Asp Trp						
	180		185		190	
His Asn Leu						
	195					

<210> 18
 <211> 1344
 <212> DNA
 <213> Plant

<220>
 <221> CDS
 <222> (1)...(1344)

<400> 18	
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Met Thr Ala Glu Asp Ile Arg Arg Arg Asp Lys Lys Thr Glu Glu Glu	
1 5 10 15	
aga aga cta aga gac acg tgg cgt aag atc caa gga gaa gac gat tgg	96
Arg Arg Leu Arg Asp Thr Trp Arg Lys Ile Gln Gly Glu Asp Asp Trp	
20 25 30	
gcc ggg tta atg gat cca atg gat cca att ctt aga tcg gag cta atc	144
Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile	
35 40 45	
cgt tac ggc gaa atg gct caa gct tgt tac gac gct ttc gat ttc gat	192
Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp	
50 55 60	
ccc gct tcc aaa tac tgc ggc acc tcc agg ttc acg cga ctc gag ttc	240
Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe	
65 70 75 80	
ttc gat tct ctc gga atg atc gat tcc ggt tac gag gtg gcg cgt tac	288
Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr	
85 90 95	
ctc tac gcg acg tcg aac atc aat ctc ccg aac ttc ttc tcg aaa tcg	336
Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser	
100 105 110	

cgg tgg tct aaa gtc tgg agc aaa aac gct aat tgg atg gga tac gtc Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val 115 120 125	384
gcc gtt tca gac gac gaa acg tct cgt aac cga ctc ggc cgc cgt gat Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp 130 135 140	432
atc gcg att gcg tgg aga gga acc gtt acg aaa ctt gaa tgg atc gcg Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala 145 150 155 160	480
gat cta aag gat tat tta aaa ccg gta acc gaa aac aag atc cga tgc Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys 165 170 175	528
ccc gac ccg gcc gtt aaa gtc gaa tcc gga ttc tta gat ctc tac act Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr 180 185 190	576
gac aaa gac aca acc tgc aaa ttc gcg aga ttc tca gcg cgt gaa cag Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln 195 200 205	624
att tta acg gag gtg aaa ccg tta gtg gaa gaa cac ggc gac gac gat Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp 210 215 220	672
gat tcc gat tta agc atc acc gtg acg gga cac agt ctc ggc ggc gcg Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala 225 230 235 240	720
tta gcg ata tta agc gcg tac gat ata gcg gag atg aga ttg aat ccg Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg 245 250 255	768
agt aag aaa ggg aaa gtg att ccg gtg acg gtg ttg aca tac gga gga Ser Lys Lys Gly Lys Val Ile Pro Val Thr Val Leu Thr Tyr Gly Gly 260 265 270	816
ccg aga gtt ggg aac gtt agg ttt agg gag agg atg gag gaa ttg gga Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu Gly 275 280 285	864
gtg aaa gtg atg aga gta gtg aat gtt cac gac gtg gtt ccc aag tcg Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys Ser 290 295 300	912
ccg gga ttg ttt ttg aac gag agt aga cct cac gcg ctg atg aag ata Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys Ile 305 310 315 320	960
gcg gag ggg ttg ccg tgg tgt tat agc cac gtg ggg gag gag ctg gcg Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu Ala 325 330 335	1008

ttg gat cat cag aac tcg ccg ttt ctt aaa cct tcc gtt gat gtt tct	1056
Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val Ser	
340 345 350	
act gct cat aat ctt gaa gct atg ctt cat tta ctt gac ggg tat cat	1104
Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr His	
355 360 365	
gga aaa gga gag aga ttt gtg ctg tcg agt ggg aga gac cat gcg cta	1152
Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala Leu	
370 375 380	
gtg aac aaa gcg tcg gac ttt ttg aaa gag cat tta caa att cca ccg	1200
Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro Pro	
385 390 395 400	
ttt tgg cgt caa gac gcg aat aaa gga atg gtt cgg aac agt gaa ggt	1248
Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu Gly	
405 410 415	
cgt tgg att caa gcc gag cgt ctc cgt ttt gag gat cat cat tct cct	1296
Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser Pro	
420 425 430	
gat atc cac cac cat ctc tct cag ctc cgt ctt gat cat cct tgt taa	1344
Asp Ile His His His Leu Ser Gln Leu Arg Leu Asp His Pro Cys *	
435 440 445	

<210> 19
 <211> 447
 <212> PRT
 <213> Plant

<400> 19

Met Thr Ala Glu Asp Ile Arg Arg Arg Asp Lys Lys Thr Glu Glu Glu	
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Arg Arg Leu Arg Asp Thr Trp Arg Lys Ile Gln Gly Glu Asp Asp Trp	
20 25 30	
Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile	
35 40 45	
Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp	
50 55 60	
Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe	
65 70 75 80	
Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr	
85 90 95	
Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser	
100 105 110	
Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val	
115 120 125	
Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp	
130 135 140	
Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala	

145		150		155		160									
Asp	Leu	Lys	Asp	Tyr	Leu	Lys	Pro	Val	Thr	Glu	Asn	Lys	Ile	Arg	Cys
		165		170		175									
Pro	Asp	Pro	Ala	Val	Lys	Val	Glu	Ser	Gly	Phe	Leu	Asp	Leu	Tyr	Thr
		180		185		190									
Asp	Lys	Asp	Thr	Thr	Cys	Lys	Phe	Ala	Arg	Phe	Ser	Ala	Arg	Glu	Gln
		195		200		205									
Ile	Leu	Thr	Glu	Val	Lys	Arg	Leu	Val	Glu	Glu	His	Gly	Asp	Asp	Asp
		210		215		220									
Asp	Ser	Asp	Leu	Ser	Ile	Thr	Val	Thr	Gly	His	Ser	Leu	Gly	Gly	Ala
		225		230		235									
Leu	Ala	Ile	Leu	Ser	Ala	Tyr	Asp	Ile	Ala	Glu	Met	Arg	Leu	Asn	Arg
		245		250		255									
Ser	Lys	Lys	Gly	Lys	Val	Ile	Pro	Val	Thr	Val	Leu	Thr	Tyr	Gly	Gly
		260		265		270									
Pro	Arg	Val	Gly	Asn	Val	Arg	Phe	Arg	Glu	Arg	Met	Glu	Glu	Leu	Gly
		275		280		285									
Val	Lys	Val	Met	Arg	Val	Val	Asn	Val	His	Asp	Val	Val	Pro	Lys	Ser
		290		295		300									
Pro	Gly	Leu	Phe	Leu	Asn	Glu	Ser	Arg	Pro	His	Ala	Leu	Met	Lys	Ile
		305		310		315									
Ala	Glu	Gly	Leu	Pro	Trp	Cys	Tyr	Ser	His	Val	Gly	Glu	Glu	Leu	Ala
		325		330		335									
Leu	Asp	His	Gln	Asn	Ser	Pro	Phe	Leu	Lys	Pro	Ser	Val	Asp	Val	Ser
		340		345		350									
Thr	Ala	His	Asn	Leu	Glu	Ala	Met	Leu	His	Leu	Leu	Asp	Gly	Tyr	His
		355		360		365									
Gly	Lys	Gly	Glu	Arg	Phe	Val	Leu	Ser	Ser	Gly	Arg	Asp	His	Ala	Leu
		370		375		380									
Val	Asn	Lys	Ala	Ser	Asp	Phe	Leu	Lys	Glu	His	Leu	Gln	Ile	Pro	Pro
		385		390		395									
Phe	Trp	Arg	Gln	Asp	Ala	Asn	Lys	Gly	Met	Val	Arg	Asn	Ser	Glu	Gly
		405		410		415									
Arg	Trp	Ile	Gln	Ala	Glu	Arg	Leu	Arg	Phe	Glu	Asp	His	His	Ser	Pro
		420		425		430									
Asp	Ile	His	His	His	Leu	Ser	Gln	Leu	Arg	Leu	Asp	His	Pro	Cys	
		435		440		445									

<210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 20
 atgtctagag aagatatgtgc gcggcga

27

<210> 21
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

• <223> Primer

<400> 21

gatgagctcg acgaagctga gagagatg

28